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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MODEL-frame+_p2n.model -DEV-x1h
-Q=/cg12_1/USPTO_spool/USO9677653/runat_20022003_164317_1369/app_query.fasta_1.839
-Q=/cg12_1/USPTO_spool/USO9677653/runat_20022003_164317_1369/app_query.fasta_1.839
-DB=Published_Applications_Na -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEX=0 -LOOPEX=0 -UNITS-bits -START=1 -END=-1 -MARTX-sblosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=USO96-1653_@CGN_1_1_35_@runat_20022003_164317_1369
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution.
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124.5
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                                                                                                                                    Score
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14:
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                                                                                                                                                             Query
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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'cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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11739
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US-09-070-927A-150
US-09-821-616-33
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     US-09-815-242-8615
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4691.643 Million cell updates/sec
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Sequence 167, App
Sequence 150, App
Sequence 33, Appl
Sequence 8615, Ap
                                                                                                                               Description
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|--|---|---|--|
| 443<br>443<br>543  | 27<br>28<br>30<br>31<br>32<br>33<br>34<br>35<br>36<br>36<br>37  | 17<br>18<br>19<br>20<br>21<br>22<br>25<br>26  | 5<br>6<br>6<br>7<br>7<br>8<br>8<br>9<br>9<br>110<br>111<br>112<br>113<br>114   |
| 104<br>103.5<br>103.5<br>103<br>103<br>103   | 106.5<br>105.5<br>105.5<br>105.5<br>105.5<br>105.5<br>105.5<br>105.6<br>105.6   | 112.5<br>111.5<br>110.5<br>110.5<br>110.5<br>110.5<br>110.5<br>109  | 13166.6111   |
| 3 3 3 3 3 3<br>0 1 1 1 1 1   |   |   |  |
| 13029<br>2757<br>88421<br>1984<br>2076<br>1965   | 32768<br>3914<br>4530<br>8772<br>8871<br>3309400<br>2448<br>4041<br>4041<br>4041<br>36778<br>36778<br>36778   | 1509<br>1708<br>4190<br>3903<br>3903<br>4260<br>4645<br>4645<br>3591<br>3663  | 81940<br>2872<br>2872<br>2872<br>2872<br>1929<br>1929<br>1959<br>1971<br>3112<br>5072<br>25165<br>2906                       |
| 10   | 10<br>10<br>10<br>10<br>10<br>10<br>10  |   |  |
| US-09-815-242-4052<br>US-09-738-626-3470<br>US-09-976-059-1<br>US-10-146-474-5<br>US-09-938-842A-1260<br>US-09-826-660-26  | 109-070-927A-39 10-044-090-148 9-738-626-207 09-788-711A-3 09-788-711A-3 09-788-721A-3 09-788-721A-3 09-815-242-405 9-861-248-36 09-861-289-36 09-861-289-36 09-860-846-5 09-860-846-5 09-860-846-5 09-860-846-5 09-860-846-5 | US-09-738-626-2545 US-09-822-830A-612 US-09-962-832-11 US-09-815-242-3848 US-09-815-242-6809 US-09-925-302-196 US-09-971-536-27 US-10-098-841-45 US-09-738-626-1  | 508B-1 380-105 -217-10 -263-10 000-1 0000-5 0000-3 0000-7 -800A-1 -090-64  |
| Sequence 4052, Ap<br>Sequence 3470, Ap<br>Sequence 1, Appli<br>Sequence 5, Appli<br>Sequence 1260, Ap<br>Sequence 26, Appl | 148<br>207,<br>3,<br>1,<br>1,<br>1,<br>36,<br>36,<br>36,<br>36,<br>36,<br>36,<br>36,<br>36,<br>36,  | Sequence 2545, Ap<br>Sequence 612, App<br>Sequence 111, App<br>Sequence 3848, Ap<br>Sequence 6809, Ap<br>Sequence 196, App<br>Sequence 27, Appl<br>Sequence 45, Appl<br>Sequence 44, Appl<br>Sequence 41, Appl1 | 1, Apr<br>1055,<br>e 1055<br>e 1055<br>1, Apr<br>5, Apr<br>5, Apr<br>7, Apr<br>7, Apr<br>1543,<br>e 640,<br>39, Ar<br>186, 2 |

## ALIGNMENTS

RESULT 1
US-09-070-927A-167
Sequence 167, Application 1
Patent No. US20020120116A1
GENERAL INFORMATION:

Application US/09070927A

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                         PRIOR
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                         APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
APPLICATION DATA: 60/046,655
                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                      STATE: Maryland
                                                                                                                                                                                                                                                                                                             CITY: Rockville
                                                                                                                                                                                                                                               20850
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Patrick J. Dillon
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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID US-09-070-927A-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 19031 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                     4846
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                                                                                                                                                                                                                                                                                                                                                                          4672
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                                 4786 AATGAAAAAGGCGGGGCTTTCACACCGGCGTTAACTTTTAGTGGTAAGTACTATGCGCAA 4845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4462 AACCGCAAAGTCACCGAGAACTTCGTAGACACCAACGGCGCTAAA------
                                                                     176
                                                                                                                                      156
                                                                                                                                                                                                                                                         132 GluIleTyrAsnGluGluCysProValValThrAspValSerValProLeuAsp----- 149
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                                                                                                                                                                                                                                                                                                                                    112 GlyGluTyrSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArg 131
   187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
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APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGRET INFORMATION:
NAME: Kenley K. HOOVET
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 ThrGlyArgGlnValSerProProAspAsnPheThrAlaAlaAlaGlnAspLeuAlaGln 58
                                                                                                                               SerIlePheSerPheProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsn 175
                                                                                                                                                                                                                                      GTGGTGTATGAAGAAGAACAGTTACGACAGTGTATCCATCAGTCGATATGAACTTTGTG 4785
                                                                                                                                                                                                                                                                                                      -----ACCAAAGCGCCAAGTTATCAAGTGACCTACGATGACAATGATGATTTGAAT 4725
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----MetProGluPheArgAsnTrpAlaLysGlyLysIleAspLeuAspSerAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerLeuAspAlaAsnThrVal-----73
IleGluTrpLeuAsn----
                                                                                                 AGTACGAGTGCGTAC-----TTAAGAACCGATTTATATGACGTGACCTCAAAAAATAAT 4899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGC---GACGCCTACACTTTCAAACAAGCAGGCACCTTACCAGACACTTACACAACAGGC 4611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ATCACACCCCCAACAGGTTTCACCCAAGGTAAAAAAAACGGTGATTACA 4554
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139.50
31.38%
18.69%
4.13%
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                                                              --LysGluMetSerLeuAspValValAsnAspLeu 186
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Matches:
Conservative:
Mismatches:
Indels:
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140
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247
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31
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| 475<br>5901 | GlyCysTyrLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSer                                  | 456<br>5875 | Оу    |
|-------------|---|-------------|-------|
| 455<br>5874 | PheGlyGlnThrValAlaAsnAsnProLysIleGluGlnSerLeuLeuLysGluThrLeu                                  | 436<br>5818 | Db Db |
| 435         | GluThrArgProSerSerArgArgLeuGluLeuProMetProProAlaAsp:::  | 419         | Qy    |
| 5817        |   | 5758        | Db    |
| 418         | ThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeu                                  | 399         | Qy    |
| 5757        |   | 5725        | Db    |
| 398         | AlavalAspGluValValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPhe                                  | 379         | Qy    |
| 5724        |   | 5665        | Db    |
| 378<br>5664 | AsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnVal   ::           ::             :: | 359<br>5605 | Оу    |
| 358         | ProAlaGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspPro                                  | 339         | Qy    |
| 5604        |   | 5578        | Db    |
| 338<br>5577 | AlaTrpGluGlnAlaSerSerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrThrPhe                                  | 319<br>5563 | Фр    |
| 318         | AlaPheValTrpAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrPro :::                                    | 301         | Qy    |
| 5562        |   | 5506        | Db    |
| 300         | ThrLeuThrPheAlaArgProSerSerAlaAlaAlaLeu   | 288         | Qy    |
| 5505        |   | 5449        | Db    |
| 287         | TyralaLeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTyralaLeuHis                                  | 268         | Qy    |
| 5448        |   | 5398        | Db    |
| 267<br>5397 | IleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGlyGln :::                              | 248<br>5365 | Qy    |
| 247         | ProAspProThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAla                                  | 228         | Qу    |
| 5364        |   | 5320        | Db    |
| 227<br>5319 | ValArgIleArgValLeuArgProThrTyrAspVal  | 216<br>5260 | Оу    |
| 215         | PheThrAsnAspThrThrTyrTyr  | 208         | Qy    |
| 5259        |   | 5200        | Db    |
| 207         | GACCCAAATGTAGCACCAGCAGAGGTTGACCTTAGTTCAGAATCTCTTAACTTGCTTAAT                                  | 201         | Qy    |
| 5199        |   | 5140        | Db    |
| 200         | AsnLeuAlaAspTrpArgTyrValVal   | 192         | Qy    |
| 5139        |   | 5080        | Db    |
| 5079        | GATAAATTAGCCATCGACCAACAACTAAAATATGTTGACAGCATTCAAT   | 5020        | - Db  |
| 5019        | TTGAAAAATATAATAATGGACAACCAATCAGTGCTACCAACAGATTACAGTTTAATGTT                                   | 4960        | Db    |

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RESULY 4
US-09-070-927A-150
; Sequence 150, Application US/09070927A
; Patent NO. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; APPLICANT: Patrick J. Dillon
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                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Enterococcus NUMBER OF SEQUENCES: 982
                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGlu-----AlaThrSerSer 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProAlaThrAspAsnPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACAACACAGCTTGAAAACAAGCCGCGGATTACTACGGTAACGGCACACGGAATCCGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysAsnGluGluIleLeuCysLeuAlaAsp------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCATCAGTGTGCCAACCTTCGAC----TTCGGCCAAGTGGGCGTTGCAGGAACTAAG 6117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAlaGlyLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGAAGTTGTAGTATTTGGTGGTATTAAAGATAGTACAGTGGATAACTTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTAGCTTAACAGCCAACACACACAGCA 6384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleIleLysSerValGlyGluThrAla 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGCGACAGACAGCTTGCCTACAGCGACCCGCTTATTATTAGGGGGCGGCGCCTGTCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAAGTTTCAGTTGCTTTCACAACTCGCGCAACAGGGAAACCAAACACTGTTTTGAAA
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                                                                                                                                                                                                                                                                                                                               ZIP:
                                                   APPLICATION NUMBER: 60/066,009 FILING DATE: 1997-11-14
                                                                                   APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
     REGISTRATION
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                     Kenley
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   NUMBER: 40,302
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SEQUENCE DESCRIPTION:
US-09-070-927A-150
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-677-653A-50 (1-647) x US-09-070-927A-150 (1-11739)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO: 150:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgAsnTrpAlaLysGlyLysIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACAAAGT----GGCACCTTGCCAGATACCTATCAAGCAGACGGCAAAAACCTATAAGTTC 9394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrValAsnGlyArgArgAsnGlnArg----
                                                                                                                    TTGAAGGAAATTGCTTATCCTGCGCAATCTCTTGAAATACTGAGTGATCGAAGTACA---
                                                                                                                                                    IleArgGluIleTyr---
                                                                                                                                                                                       ValAsp------
                                                                                                                                                                                                                                                        GATGCTTCAACAATTGGGTTGACTTATGACAAATGGCGTGGGGGAGTTGTTAACAAATAAT 9634
                                                                                                                                                                                                                                                                                          SerAlaArgAlaValGly---GluTyrSerLySIleProAspGlyLeuValLysPheSer 125
                                                                                                                                                                                                                                                                                                                                                                                               TATGCGGTGACTTATAACAATGATGATGATTTGACGGTGGTGTATGAGGAGATTGAGTTT 9514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGGTTGGTACAAAGGCAAAACCAAGCCAAACCATTGACCACCACAAAGCACCAAGC 9454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGATTCACACAAGGAAAGCGAACGGTT------ATTAATAGTGAAGCGTACACTTTT 9337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnPheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsnThrValThrPhe 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACAAAAAGCTTTATGAGAATTTTGTTAATAGTAACGGACAAAAATTACACCACCATCA
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                                                                                                                                                                                                                                                                                                                            TTTGACTTCCCAGCGCTGACCTATCAATTCGGGTTCGTGGACGAGTCTGGCAAACGAGTA 9574
                                                                                                                                                                                                                                                                                                                                                            ---AspSerAspSerIleGlyTrpTyrPheLysTyrLeuAspProAlaGlyAlaThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProAlaAsnIleSerSerMetProGlu---
                                                                                  LeuAspGlyArgGlnTrpSerLeuSerIlePheSerPheProMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8504
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                                                 -CAATATAGTGCGGCTAATTTAACCTTTACACTGCCCAAATACTATGGG
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                                                                                                                                                    -AsnGluGluCysProValValThrAspValSerValPro
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Indels:
-PheArgThrAlaTyrValAlaValAlaAsn
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| 447<br>10794 | -GluLeuProMetProProAlaAspPheGlyGlnThrValAlaAsnAsnProLysIleGl ::::::  | 428<br>10741        | Фр             |
|--------------|--|---------------------|----------------|
| 427<br>10740 | LeuGluThrargProSerSerArgArgLeu   | 418<br>10681        | ρb             |
| 417<br>10680 | rAsn      AlaTyrThrAsnThrValPheArgAsnThrLeu         :::                     :::                     TGACATTGCTAATAGAGGGTACGCATTAAATAACTTGGATATTACCAATCAAATGAAATA | 405<br>10621        | Db Oy          |
| 405<br>10620 | roThrPheThrValArgValPro  | 392<br>10565        | B 8            |
| 392<br>10564 | lThrAsnAsnPr<br>      <br>GACAAATAAGTA   | 377<br>10510        | р Q            |
| 376<br>10509 | .spGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArg<br>  | or or               | P              |
| 359<br>10449 | pProA<br>AACTC   | 339<br>10390        | ۾<br>کو        |
| 339<br>10389 | UThrTrpArgH1sAsnGly  | 329<br>10330        | Оу             |
| 329<br>10329 | .uGlnAlaS<br>  | 314<br>10275        | Db Qy          |
| 314<br>10274 | alTrpAl  | 294<br>10253        | DP GA          |
| 294<br>10252 | >> ∙∙ α  | 274<br>10196        | do<br>Qy       |
| 274<br>10195 | ProThrLeuValAspGlnGlyPheTrpIleGlyGlyGlnTyrAlaLeuThrPro-ThrSe   | 255<br>10148        | рβ             |
| 254<br>10147 | LeuThrTyrLysAlaIleThr  | 243<br>10088        | pb Qy          |
| 242<br>10087 | rGluGlyLeuValA   | 223<br>10073        | Š<br>Š         |
| 222<br>10072 | GluGlnTrpIleAsnPheThrAsnAspThrThrTyrTyrValArgIleArgValLeuArg   | 203<br>10028        | р Q            |
| 202<br>10027 | ATTCCAGCAGCACCAATCGATGTTCAGGTGCCTGCTTACTTGCGAGAGATTGTCTATAAT   | 19 <b>7</b><br>9968 | Оb             |
| 196<br>9967  | UAlaAspTrp   | 0 9                 | Db Qy          |
| 192<br>9907  | etSerLeuAspValValAsnAspLeuIleGluTrpL<br>   | 173<br>9857         | Q <sub>Q</sub> |
| œ            | TCAGTGTTTATAACAAGAGTGGTACTTTTGATGCAGGCTACCTG   | 0                   | Db             |

|                  | UMBER: EARLIER APPLIC<br>EARLIER FILING DATE:<br>S: 34<br>or Windows Version 3. | ING DATE: SEQ ID N FastSEQ                                    | PRIOR APP<br>PRIOR FIL<br>NUMBER OF<br>SOFTWARE: |                   |
|------------------|---|---|--|-------------------|
|                  | EARLIER APPLICATION NUMBER: 08/979,6<br>ER FILING DATE: 1997-11-26              |   | RIOR   |                   |
|                  | EARLIER   | ATION   |  |                   |
|                  | EARLIER APPLICAT  | APPLICATION<br>FILING DATE:                                   |  |                   |
|                  | EARLIER   | APPLICATION NUMBER:   | PRIOR !  |                   |
|                  | EARLIER APPLICAT R FILING DATE: 19  | APPLICATION NUMBER: FILING DATE: EARLIE                       | PRIOR /  |                   |
|                  | EARLIER APPLICATION NUMBER: 09/19 R FILING DATE: 1998-11-24                     | APPLICATION NUMBER: FILING DATE: EARLIE                       | PRIOR I  |                   |
|                  |   | NT APPLICATION NUMBER:<br>NT FILING DATE: 2001-               | CURRENT  |                   |
|                  | ck, Jan<br>: Thermostable Glucoamylase<br>79 200-US                             | GEFERENCE: 5279.  | TITLE OF I                                       |                   |
|                  | . Bjarne R.<br>n, Ruby  | z   | APPLICANT:                                       |                   |
|                  | us/09821616<br>0030027290A1   | -616-33<br>e 33, Applicat:<br>tion No. US200:<br>INFORMATION: | SULT 3 ·09-821-( Sequence Publicati              | RES<br>US-<br>; P |
|                  | ACTAGOGGOGATGTCACOTGGOGGOGACAATTACCA 11342                                      | GTO   | 11293  | Db                |
|                  | AlaAlaGlnSe   | yGluThrAla-   | 605  | Qy                |
| 11292            | ACGGCGATTTATAAGGAAGAAGTGCCCAAAGCAGTGTCGCTTTAACGCGCACTACCGC                      | GACGGCGATTT   | 11233  | Db                |
| 1 605            | euLysSerGluAlaThrSerSerIleIleLysSerValGl  | uSerSerValLeuLysS   | 588  | Qy                |
| :<br>F 11232     |   | <br>ATATAACACAACT   | 11200  | Db                |
| 588              | TyrProAlaThrAspAsnPheAlaAlaAlaValSerAlaPheAlaAlaAsnMetLe                        | lTyrProAlai   | 569  | Qy                |
| C 11199          | TTAACAACCAGCACTACGCCAAC   |   | 11177  | DЬ                |
| g 569            | uLeuLysAsnGluGluIleLeuCysLeuAlaAspAspLeuAlaThrArgLeuThrGlyVa                    | uLeuLysAsn(   | 549  | Ωу                |
| - 11176          | TGGTACAAAGGCAAAACGAAGCCTAATACT  | TGGTAC  | 11146  | Дb                |
| e 549            | GluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAlaGlyLe                           | yTrpGluc  | 530  | Qγ                |
| 3 11145          | AAAAGCCTTGCCAGCAACTTATACCGCAGGTGGCAAGACCTATACTTTCCAAGG                          | AGCCGCAAAA  | 11086  | Д                 |
| 1 530            | ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyrGlnGl                     | -valAlaHis  | 511  | Qy                |
| c 11085          | ACCAACAGGCTTCACCCAAGGCAACAAAATACCCATGACTAGCAACACCTTCAAGTACAC                    | ACCAACAGGCT   | 11026  | 뫄                 |
| - 510            |   |   | 510  | Qy                |
| 11025            | AGTCACCCGTAAACAAGTCACCGAAAAACTTTGTTGATGCCAAACGGTGCCAAAATCACCGC                  | AGTCACCCGT!   | 10966  | рь                |
| - 510            |   | rGlyIleArg/   | 497  | Qy                |
| A 10965          | TACTCCAGACTA  | ATTATTCGGGTTTGATGG  | 10915  | Дb                |
| h 497            | snAsnproGlyTyrGluArgThrArgAspLeuProAsp  | al  | 479  | Qy                |
| G 10914          | ATATAGTTCCCAAAATGTTATTGTTAGCAGAAAGTGGCAGTTTTTCAAG                               | AACGTTTTCGC   | 10855  | DЬ                |
| 1 479            | dIn   | oValPheGln-   | 467  | Qγ                |
| r 467<br>G 10854 | uGlnSerLeuLeuLysGluThrLeuGlyCysTyrLeuValHisSerLysMetArgAsnPr<br>::::::: :::     | uGlnSerLeuL<br>:::::::<br>TAAAACATTTG                         | 447<br>10795                                     | oy<br>Qy          |

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; ORGANISM: Talaromyces emersonii
US-09-821-616-33
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                                2114 TCTAGGAGAAATATACTCCCTCAGA------CGGCTCTCTTACCGAACAATTCT 216:
                                                                                                                                                             1994 TCCACGACTTTCAACGACATCATCTCGGCCGTCCAGACGTATGGTGATGGATATCTGAGT 2053
                                                                                                                                                                                                                                                                                             1877 CTTTACGACGCCATCTACCAGTGGAAGAAGATCGGCTCGATAAGTATCACGGACGTTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 TyrAsnGluGluCysProValValThrAspValSerValProLeuAspGlyArg----- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 TyrSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArgGluIle 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 pPro-ThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAla---I 248
                                                                                                                                                                                                                                                           160 PheProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGluMetSer 179
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                                                      rAsnAspThrThrTyrTyrValArgIleArgValLeuArgProThrTyrAspValProAs
                                                                                                                           -------ArgTyrValValAspSerGlu------GlnTrp-IleAsnPheTh
                                                                                                                                                                                  -----SerLeuSerIlePheSer 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCGCCGGAGGCTGTGACGACTCGACCTTCCAGCCGTGTTCGGCCCGTGCCTTGGCAAAT 1726
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| RDD   | ď             | Qy           | рь                    | Qy  | Db Qq   | Db :  | Qy  | Qу<br>Дъ  | Dр   | Qy  | Qу<br>Дъ   | Db   | Qy              | d<br>Q  | Db                              | Qy .   | 망    | VQ<br>VQ | Db   |
|---|---------------|--------------|-----------------------|---|---|---|---|---|------|---|--|--|-----------------|---|---------------------------------|--|------|----------|------|
| RESULT 4 US-09-815-24 Sequence 8 Patent No. GENERAL IN APPLICANT FILE OF FILE REFE CURRENT A CURRENT A CURRENT A CURRENT A CURRENT A FILE PRIOR APP   | 2693          | 439          | 2642                  | 419   | 403<br>2582   | 2537  | 383   | 363<br>2501   | 2483 | 343   | 323<br>2423  | 2363   | 308             | 288<br>2303   | 2254                            | 268  | 2222 | 248      | 2162 |
| Ce 8615, Application US/09815242  NO. US20020661569A1  I INFORMATION: CANT: Haselbeck, Robert CANT: Ohlsen, Kari L. CANT: Cyskind, Judith W. CANT: Trawick, John D. CANT: Trawick, John D. CANT: Yamamoto, Robert T. CANT: Yamamoto, Robert T. CANT: Xu, H. Howard  OF INVENTION: Identification of Essential Genes in OF INVENTION: Identification of Essential Genes in OF INVENTION NUMBER: US/09/815,242 NT FILING DATE: 2000-03-21 APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-23 APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-25 APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-25 APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26 APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26 APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-10-23 | CTACCGCC 2700 | hrValAla 441 | GTCGTACACGGTCCCAGCGTA | luThrargProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnT 43 | roProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuG 41 | TTACACCAACAGCAACCGCTCTGGTACGTGACCGTCAATCTGC 2 | alValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrValArgValP 40 | rpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaValAspGluV 38 | N    | lSerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAsp | laSerSerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrThrPheProAlaGlySerV 343 ::: ::::::::::::::::::::::::::::::: | GCTCTGGCAGCTCAACAACCACCAGTAGCGCCCCATGCACCACTCCTACCTCTGTGGCTG 242 | AlaProAlaGlyThr | hrLeuThrPheAlaArgProSerSerAlaAlaAlaLeuAlaPheValTrpAlaGlyLeuP 308 :: | : : : : : : : : : : : : : : : : | yrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHisT 288 | N    |          |      |
|   |               |              | 92                    | 39  | ا<br>541  | 81  | 03  | 183   | 500  | ŭ   | 343<br>2482  | 122  | ä               | 62  | 2302                            | œ  | 53   | 83       | 2221 |

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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 8615
LENGTH: 7035
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; NAME/KEY: CDS
; LOCATION: (1)...(7035)
US-09-815-242-8615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        880 CAAAAAGGTGCC-----AITACATTAGGAACACGTATTGACTCTAATAAGAGTTTTCAT 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 GlnValSerProProAspAsnPheThrAlaAla-----AlaGlnAspLeuAlaGln
TyrValAlaValAlaAsnValGluAsnLysGluMetSerLeuAspValValAsnAspLeu ::::::||| :::|||
                                                                                                                                                                                                                                                                                                                      ACATCTACGCCAAATTCATCAGCAAAAGGCGAAAGCTGACCCATCTAATGTAGCTGGTGGA 1167
                                                                                                                                                                                                                                                                                                                                                     ProAlaGlyAlaThrGluSerAlaArgAlaValGlyGluTyrSerLysIle-----
                                                   AAATATGCAGGTCAAACATGGACACGTAATATT--
                                                                    GATTTTGATATTAAT-----TATAATGGTGATACAAAAGTTATGACC------GTT 1332
                                                                                                                                                AspAlaGluIleArgGluIleTyrAsnGluGluCysProValValThrAspValSerVal 146
                                                                                                                                                                                    GGTGCGTTTGGTGCCTTTGTAACAACAGATAGTTATGGTGTTGCATCAACATATACATCA 1227
                                                                                                                                                                                                                                                                                                                                                                                        GCAGTAGGTATTGGTGGCTTAAGTAACGCATTTGGCTTCAAATTAGATACGTATCACAAT 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGGTATCGGTTTTGCCCTTTTCACCAGGTGTATTAGGTGAAACAGGGTTAAACGGTGCC 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspSerIleGlyTrpTyrPheLys------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeuAspAlaAsnThrValThrPheProAlaAsnIleSerSerMetProGluPheArg 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTAATGCCACTTATGACCAAAGTACAGGGGTCGTAACGTTAACGCAAGATACAACAAGC
                                                                                                                                                                                                                   ----ProAspGlyLeuValLysPheSerVal---
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| Db | 1372 | TGGATTGCGAAAAGTGGTACGACCAACTTTTCATTATCAAT-GACAGCCTCAAC 1424        |    |
|----|------|--|----|
| Qy | 187  | IleGluTrpLeuAsnAsnLeuAlaAspTrpArgTyrValValAspSerGluGlnTrpIle 206   |    |
| рb | 1425 | GGTGGCGCGAC 1436   | ٥. |
| Qy | 207  | AsnPheThrAsnAspThrThrTyrTyrValArgIle···ArgValLeuArgProThrTyr 225   |    |
| Db | 1437 | AAATTTACAACAAGTACAATTTGGAACATTCGAATATACAGAATCTGCTGTTACACAAGT 1496  |    |
| Qy | 226  | AspVal-ProAspProThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTy 245   |    |
| Db | 1497 | GAGATACGTTGATGTAACAACAGGT 152:                                     | •  |
| Ωу | 245  | rLysalaIleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGl 265   |    |
| Дb | 1522 | - AAAGATATTATTCCCCCAAAAACATATTCTGGAAATGTTGATCAAGTCGTGACAATCGA 1580 | _  |
| Qy | 265  | yGlyGlnTyrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTy 284      |    |
| Ф  | 1581 | TAATCAACAATCTGCATTGACTGCTAAAGGATATAACTACACATCTGTCGATAGTTCATA 1640  | -  |
| Qy | 284  | rAlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAl 298                     |    |
| Db | 1641 | TGCATCAACTTATAATGATACAAATAAAACTGTAAAAAATGACGAATGCTGGACAATCAGT 1700 | _  |
| Qy | 298  | aAlaLeuAlaPheValTrpAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrPr 318   |    |
| Db | 1701 | GACATATTATTTACTGATGTAAAAGCACCAACTGTAACTGTAGGCAATCA 1751            |    |
| Qy | 318  | oAlaTrpGluGlnAlaSerSerGlyGlyTyrLeuThrTrpArgHisAsnGlyTh 336         |    |
| DЬ | 1752 | AACCATTGAAGTGGGTAAAACAATGAATCCTATTGTGTTGACTACAACAGATAATGGTAC 181:  | •  |
| Qy | 336  | rThrPheProAlaGlySerTyalSerTyrValLeuProGluGlyPheAlaLeuGluArgTy 356  |    |
| ДĎ | 1812 | AGGGACTGTGACAAATACAGTTACAGGATTACCAAGCGGATTAAGTTA 1859              | _  |
| Qy | 356  | rAspProAsnAspGlySer 362  |    |
| DЪ | 1860 | TGATAGTGCAACGAATTCAATCATTGGGACACCAACAAAATTGGTCAATCAA               | _  |
| Qy | 363  | TrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVa 380          |    |
| Db | 1920 | AGTAGTATCTACTGACCAAGCAAATAACAAATCGACGACAACTTTTACAATAAATGTTGT 1979  | -  |
| Qy | 380  | lAspGluValValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrVa 400   |    |
| Db | 1980 | GGATACGACAGCACCAACAGTGACGCCAATAGGAGATAAATCAGCAGCAGTTTTTTCTCC 2039  |    |
| Qy | 400  | lArgValPro   |    |
| Db | 2040 | AATATCACCGATTAATATTGCTACGCAGGACAATAGTGGTAATGCAGTAACAAATACAGT 2099  |    |
| Оу | 412  | lPheArgAsnThrLeuLeuGluThrArgProSerSerArgArgLeuGluLeuProMetPr 432   |    |
| DЬ | 2100 |  |    |
| Qy | 432  | oProAlaAspPheGlyGlnThrValAlaAsnAsnProLysIleGluGlnSerLeuLeuLy 452   | •  |
| DЪ | 2131 | AGCACAAATAATACTATTAGTGGTACACCA2160                                 |    |
| Qy | 452  | sGluThrLeuGlyCysTyrLeuValHisSerLysMetArgAsnProValPheGlnLeuTh 472   |    |
| DЪ | 2161 | ACAAACATTGGTACAAGTACTATTACAATCGT 2192                              |    |
| Qy | 472  | eGlyAlaValSerPheAsnAsnProGlyTyrGluArgThr/                          |    |
| DЪ | 2193 | CAACCACTTTAAATATGA   |    |
| Qy | 492  | LeuProAspTyrThrGlyIleArgAspSerPheAspGlnAsnMetSe                    |    |
| 뮹  | 2253 | GTGATTCCGTATCAACATCGGGAAGTACCCAACAATCACAAAGTGTGTCA                 |    |

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US-09-759-508B-1
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                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09759508B
Publication No. US20020182599A1
GENERAL INFORMATION:
APPLICANT: Fishman, Mark C.
TITLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
FILE REFERENCE: 00786/381002
CURRENT APPLICATION NUMBER: US/09/759,508B
CURRENT FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 81940
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (133)..(80910)
OTHER INFORMATION:
                                                                                                                            64990 ATAAACGGCAATGAATACCAATTCCGTGTTTCTGCAGTTAACAAGTTTGGTGTTGGCAGG
                                                      65050 -----CCACTTGATTCTGATCCAGTGGTTGCTCAAATACAATATACTGTTCCTGAT 65100
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2604 TACATCTGATTCATTGCGTACATCAACATCGTTAAGTGATTCAGTAAGCATGAGTACATC 2663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2544 ATTAAGCGATTTTATTTCGAACTCTAGCAGTACTGAAAAATCAGAGAGTGTCTCAACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2490 GAATTCACAAAGTGTATCATCAAGCATGTCAGGTTCAGTTAGT-----AAATCAACATC 2543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2433 GTCA---TTAAGCACATCTGAAAGTAATAGTGTATCAAGCTCAACAAGCACAAGTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2373 ATCAGCTAGTACCTCGAAATCGACAAGTGTAAGCCTATCTGATTCTGTGAGTGCATCTAA 2432
                                                                                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627 oGlyLysIleAla 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               607 rAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuProGlyLeuLeuMetSerValPr 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587 tLeuSerSerValLeuLysSerGluAlaThrSerSerIleIleLysSerValGlyGluTh 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             567 rGlyValTyrProAlaThrAspAsnPheAlaAlaAlaValSerAlaPheAlaAlaAsnMe 587
42 GlnValSerProProAspAsnPheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAsp
                                                                                                                                                            29 ValAsnGlyArgAsgAsnGlnArgArg------ArgThrGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rTyrGlnGlyTrpGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAl 547
                                                                                                                                                                                                                                          5.96
117.50
31.72%
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Matches:
Conservative:
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Indels:
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125
65
218
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                  81
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| 66138         | CATTATGTGGTAGAGAAACGAGAGGCAAGTCGCCGTAGTTGGCAGGTTATCAGT             | 66085 | Db   |
|---------------|--|-------|------|
| 363           | heAlaLeuGluArgTyrAspProAsnAspGlySerTrp                             | 348   | Qy   |
| 66084         | GATGCCCCTCTTCTTGACGGTGCTGCCCGAATCCAT                               | 66037 | рь   |
| 347           | \rgHisAsnGlyThrThrPheProAlaGlySerValSerTyrValLeu                   | 328   | Qy   |
| 66036         | CTCCAGGCCCACCTGGCCCAATTACCTTCAAAGATGTGACCCGGGGATCTGCT              | œ     | Db   |
| 327           | hrAlaProAlaGlyThrProAlaTrpGluGlnAlaSerSerGlyGly                    | 309   | Qy   |
| UI (          | AACAACAGTGGTAGTAAGTCAATCACATTCACCGTGAAAGTGCTAGAC                   | ω     | B .  |
| $\rightarrow$ | PardDroserseral aal aa lac   Allea   ArdDroserseral ac   VI en Dro | 389   | 2    |
| Ŭi d          | ATTCCTTCAGCACCCTCACTGTGGAAAACTGCAACAGAAATGATGCAGGGAAATATATACC      | 65863 | 문    |
| 288           | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,                               | ນຸ້ອ  | 2    |
| 65862         | ACAGCTGTGTGGAGCAACCCAGACTCTAACCTTAGCCTTCGGGCTGATATCCATACAACA       | 65803 | фq   |
| 287           | ThrSerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHis                      | 273   | Qy   |
| 65802         | GTTGTTAGAGCTGGGGCCAGTATTCGCCTCTTCATTGCCTACCAAGGTAGACCTACTCCT       | 65743 | Db   |
| 272           | LeuValAspGlnGlyPheTrpIleGlyGlyGlnTyrAlaLeuThrPro                   | 257   | Qy   |
| 65742         | GACCGGTTAACAGCTCCTGAGTTAGACATAGATGCAAACTTCAAACAGACTCAT             | 65689 | DЬ   |
| 256           | SerAspTyrArgLeuThrTyrLysAlaIleThrCysGluAlaAsnMetProThr             | 239   | Оу   |
| 65688         | CTGGCACAATTAAAGCAGTT   | 65632 | Дb   |
| 238           |  | 221   | Qy   |
| 65631         | ACAAGATATACAGTCACTGATCTACAAGCAGGTGAAGAATTACAAATTCCGAGTTAGTGCT      | 65572 | Ф    |
| 220           |  | 208   | Qy   |
| 65571         | ATGTGTAAGACCGACTTAGGAGACTGGCACAAGGTGAATGCAGAGGCATGTGTGAAA          | 65515 | Дb   |
| 207           |  | 189   | Qy   |
| 65514         | GATGGTGGCATGGAAATAATTGGGTATATTATTGAA                               | 65479 | Db   |
| 188           |  | 169   | Qy   |
| 65478         | GTGAGCTTAGAATGGTCCAAACCAGTGTTT                                     | 65449 | Db   |
| 168           |  | 149   | Qy   |
| 65448         | CCCGTCAACCCACGGTCCTCCCACAGTGGTCAAAGTAACAGACACATCAAAGACAACT         | 65389 | Дb   |
| 148           | ValValThrAspValSerValProLeu  | 133   | Qy   |
| 65388         | GAAAATGCTGCAGGAGTTGGACCTGCAAGTGGCATCTCAAGACTCATTAAATGTAGAGAG       | 65329 | DЬ   |
| 132           | gGlu   | 129   | Qy   |
| 65328         | :::  | 65269 | Db . |
| 128           | ValLysPheSerValAspAla  | 122   | Qy   |
| 65268         | AGAAGAGAAAAGAAAGCACAAGATGGGTAAAAGTGATCAGCAAACGACCAATCTCTGAA        | 65209 | рь   |
| 121           |  | 102   | Qy   |
| 65208         |  | 65161 | Db   |
| 101           | LysGlyLysIleAspLeuAspSerAspSerIleGlyTrpTyrPheLysTyrLeuAspPro       | 82    | Qy   |
| 65160         | GCCCCTGGCATTCCAGAACCTAGCAACATAACAGGCAACAGCATTACCCTGACATGGGCA       | 65101 | рь   |

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APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1055
LENGTH: 2872
TYPE: DNA
ORGANISM: Homo sapiens
US-10-025-380-1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-025-380-1055; Sequence 1055, Application US/10025380; Publication No. US20020182191A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66550 ATCATTAAGGAGCCTCAAATCGAGCCCACTGCTGACCTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66490 CGTGTGAAGGCCAAGAATGATGCTGGCTATAGTGAACCCAGAGAAGCCTTCTCTTCTGTC 66549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66436 AAACAGCTAACTTTCACAGTAGAGCGTCTTGTTGAGAAAACTGAA-----TATGAATTC 66489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66376 GGCTACCTGCTTGAAATGAGACAAAAGGGATCTGACCTCTGGGTTGAAGCTGGTCACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66316 AAATCCTCCGCAGTCTTAGCTTGGCTTAAACCTGACCACGATGGAGGCAGCCGGATCACT 66375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66139 GAAAAATGCACTCGTCAGATCTTCAAGGTCAATGACCTGGCCGAA----GGTGTTCCGTAC 66195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 SerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAspTyrThrGlyIle 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 Lys------IleGluGlnSerLeuLeuLysGluThrLeuGlyCysTyrLeuVal 460
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Wang, Tongtong
Jiang, Yuqiu
Smith, Carole L.
King, Gordon E.
Wang, Aljun
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Benson, Darin R.
Meagher, Madeleine Joy
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|            | TyrLeuValHi 461   | 458                                     | Qy        |
|------------|---|---|-----------|
| iw<br>,    | AAGCTCAGGCGTCAGCGAAGAATCCAGCACATCCCACAGTCAACCGAGGCTCAACGCACAC 2513  | 2454                                    | Db        |
|            | aAsnAsnProLysIleGluGlnS   | 440                                     | Qy        |
| ω̈         | TAGCCCCAGATCACCAGATGCAACACTCTCACCTGCAACCACAAC 2453  | 2409                                    | Db        |
| •          | oSer  | 420                                     | Оу        |
| 8          | AACTTTACCCGGCAGTCCCACAACACCAAGCCTCAGTGAGAAATCAACCACCTTCTACAC 2408   | 2349                                    | Дb        |
| -          | lArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuGluTh 420  | 400                                     | νo        |
| 80         | TGGCCTCGTTGGAGAATCCACACCTCACGCCTCAGTCCAAGCTCAACCGAAACAAC 234  | 2289                                    | g.        |
| _          | 4   | 380                                     | ογ        |
| 8          | PGLYSETTETHERANGENVALASERALAGIYASPTHEVALTHERANGGINVALALAVA 380  | 2248                                    | da<br>Ka  |
| 7          | AGCTCA  | 2241                                    | Db        |
| J          | aGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspProAsnAs 360 :  | 340                                     | у         |
| 9          | AGGGTTACCTGCCACACTCACAACCGCAGACCTCGGTGAGGAATCAACTACCTTTCCCAG 2240   | 2181                                    | מם        |
| J          | aSerSerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrThrPheProAl 340   | 323                                     | Qy        |
| ő          | CACCTCGGGCCTCACTGAAGAATCTACAGCCTTCCCCGGCAGCCCAGCCTCCACCCAAAC 2180   | 2121                                    | qa        |
| Č          | 2 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7   | 303                                     | ָ<br>בּ   |
| , w        | rLeuThrPhe···AlaArgProSerSerAlaAlaAlaLeuAlaPhe······va 303  | 288                                     | 2 09      |
| 00         | CTCAACTGAAACCACAGTGTTCCCTCGCAGCACCACAACCTCAGTTCGTGGTGAAGAGCC 2060   | 2001                                    | מם        |
| w          | ThrSerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHisTh 288   | 7 273                                   | οy        |
| 00 '       |   | 195                                     | Db .      |
| ~ ;        | Met DroThrienValAssGlnGlvPheTrsIleGlvGlvGlnTvrAlaIenvThrDro 272   | 25                                      | 2 !       |
| <b>.</b> 0 | TyrLysAlaIleThrCysGlu-AlaAs 253 CACCACCTCCCGTAGCCAACCAGGTTCTACTCACTCAACAGTACCACCACCACCACCACCACCACCACCACCACCACCACC   | 245                                     | Db<br>Db  |
| 39         | CCAACCACAACACTCTCACCTGCCAGCATGACAAGCCTAGGCGTCGGTGAAGAATC 188  | 1830                                    | ДD        |
| *-         | LeuThr 244  | 243                                     | уо        |
| 29         | :::<br>CCACCTTCTACAGCAGCCCCAG 182   | 1773                                    | DЬ        |
|            | erAspTyrA   | 223                                     | δ         |
| 72         | 177   | _                                       | Db        |
| ~          | GluGlnTrpIleAsnPheThrAsnAspThrThrTyrTyrValArgIleArgValLeuArg 222  | 203                                     | γQ        |
| 36         | TCTACAACCTCACGCAT 173   | 167                                     | da        |
| ~          | 653A-50 (1-647) x US-10-025-380-1055 (1-2872)<br>AsnAspLeuTleGluTrpLeuAsnAsnLeuAlaAspTrpArgTyrValValAspSer 202  | 3-09-677-                               | ov Sin    |
|            | ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( )   | •                                       |           |
|            | Score: 117.00 Matches: 91 Percent Similarity: 33.26% Conservative: 54 Best Local Similarity: 20.87% Mismatches: 170 Query Match: 9.47% Indels: 121 DB: 9 Gabs: 17 | Score: Percent Si Best Local Query Matc | ក្ខង្គង់ល |

| US-09-677-653A-50 (1-647) x US-09-922-217-1055 (1-2872)  Qy 184 ASNASPLeuIleGluTrpLeuASNASNLeuAlaASpTrpArgTyrValValAspSer 202 | OKSANIAM: HOMO SAPIENS   | FILE REFERENCE: 210121.471C13 ; CURRENT APPLICATION NUMBER: US/09/922,217 ; CURRENT FILING DATE: 2001-08-03 ; NUMBER OF SEQ ID NOS: 1124 ; SOFTWARE: FASTSEQ for Windows Version 4.0 ; SEQ ID NO 1055 ; LENGTH: 2872 ; TYPE: DNA | APPLICANT: Wang, Tongtong APPLICANT: Wang, Tongtong APPLICANT: Wang, Tongtong APPLICANT: Smith, Carole Lynn APPLICANT: King, Gordon E. APPLICANT: King, Gordon E. APPLICANT: Wang, Aijun APPLICANT: Clapper, Jonathan D. TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE | LO.  | Qy 505 nAsnMetSerThrAlaValAlaHisPheArgSerLeuSerHisSerCysSerIleValTh 525 ::::::    ::: | Db 2514 AACAGCGTTCCCTGACAGCACCACCACCTCAGGCCTCAGGAACCTAAAACTTCCCA 2573  Qy 461 sSerlysMetArgAsnProValPheGlnLeuThrProAlaSerSerPh 477 |
|---|--|--|--|--|---|--|
| 477 eGlyAlaValSer   | Qy 440 IALASHASHPTOLYSIIGGUGINSETLEGULPULYSGIUTHTLEUGIYCYS 457   Company | 400 largvalproproSerAsnAlaTyrThAsnThrValPheArgAsnThrLeuLeuGluTh ::::   | 60 pGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVa  | 202 ITERATELY PERFORMANCE OF THE FORTEST FOR THE FORTEST FOR THE FORTEST FORTE | 2/3   | 243 LeuThr   |

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TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Weagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR FILLE REFERENCE: 210121, 471C12
CURRENT APPLICATION NUMBER: US/09/833, 263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
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APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
                                                 SEQ ID NO 1
LENGTH: 1929
                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09554000 Patent No. US20020165364A1
                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/554,000 CURRENT FILING DATE: 2000-04-20
                                                                                                                         PRIOR APPLICATION NUMBER: 08/818,252 PRIOR FILING DATE: 1997-03-14
                                                                                       SOFTWARE: FastSEQ
                                                                                                          NUMBER OF SEQ ID NOS:
ORGANISM: Aequorea victoria FEATURE:
                                    TYPE: DNA
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                       pTyrArgLeuThrTyrLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspGl 260
                                                                                                        lLeuArgProThrTyrAspValProAspProThrGluGlyLeuValArgThrValSerAs 240
                                                                                                                                               CGGCGAGGGC-----GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTT 1349
                                                                                                                                                                                                                          GGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TyrAsnGluGluCysProValValThrAspValSerValProLeuAspGlyAr 151
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| SATTCCAGAGTTCAAAGAACCCTTCTCATTATTCCACAAAGATGGGGCACCACT 77  AA PAGAGTATH-CAJATGGLIVAL   |
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| <br>ф                                | 1620                                  | CCTGGGGCACA 163   | 30 |
|--------------------------------------|---------------------------------------|---|----|
| <br>Qy                               | 357                                   | AspPheAlaSerAlaGlyAspThr  | -  |
| Db                                   | 1631                                  | AGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGA 167  | 76 |
| Qy                                   | 374                                   | hrPheArgGlnValAlaValAspGluValValValThrAsnAsnProAlaGlyG 392  | io |
| рь                                   | 1677                                  | GGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAG 17  | 36 |
| Qy                                   | 392                                   | lyGlySerAlaProThrPheThrValArgValProProSer 405   |    |
| ф                                    | 1737                                  | CGTGCAGCTCGCCGACCACCTACCAGCAGAACACCCCCATCG 1777   |    |
| RESU<br>US-0                         | SULT 11<br>3-09-554-000-              | 000-3<br>3, Application US/09554000   |    |
| G P G                                | Patent No.<br>GENERAL IN              | VO. US2020165364A1 INFORMATION:   |    |
| <br>> >                              | PPLICA                                |   |    |
| <br>144                              | TILE O                                | TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR TITLE OF INVENTION: DETECTION OF ANALYTES                       |    |
| <br>G =                              | TLE RE                                | FERENCE: 07257/042001 APPLICATION NUMBER: US/09/554.000   |    |
| <br>                                 | URRENT                                | 252   |    |
| <br>o z o                            | PRIOR FILI                            | ILING DATE: 1997-03-14 OF SEQ ID NOS: 56 E. Fastero for windows Version 4 0   |    |
| SE :                                 | LENGTH:                               | 959   |    |
|                                      | ORGANISM:<br>FEATURE:                 | IUNA<br>ISM: Aequorea victoria<br>RE:   |    |
| 1                                    | NAME/KEY:<br>LOCATION:<br>-09-554-000 | EY: CDS<br>ON: (0)(1956)<br>000-3   |    |
| Alignm<br>Pred.<br>Score:            | Alignment<br>Pred. No.:<br>Score:     | 0.0261 Length:<br>116.50 Matches:   |    |
| Percent<br>Best Lo<br>Query M<br>DB: | ent Si<br>Local<br>Y Matc             | ent Similarity: 36.46% Conservative: 61 Local Similarity: 23.14% Mismatches: 137 Match: 9 Gaps: 26                  |    |
| us-o                                 | 9-677-                                | 653A-50 (1-647) x US-09-554-000-3 (1-1959)  |    |
| P 04                                 | 2                                     | н   |    |
| Db                                   | 657                                   | GGTCCTGCTGGAGTTCGTGACCGCCGCCCCGCATGCATGACCAACTGACAGAAGAGCA /13  | _  |
| Db Qy                                | 18 .<br>714                           | ArgAsnValArgValSerAlaAsnThrValThrValAsnGlyArgArgAsn 34GATTGCAGAGTTCAAAGAAGCCTTCTCATTATTCGACAAGGATGGGGACGGCACCAT 770 | -  |
| Qy                                   | 35                                    | GlnArgArgArgThr-GlyArgGlnValSerProProAspAsnPh 49  |    |
| Db                                   | 771                                   | GGCACCGTTATGAGGTCGCTTGGACAA   | ٠. |
| Qy                                   | 49                                    | eThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsnThrValTh 66  |    |
| Db                                   | 826                                   | GCAGAATTGCAGGATATGATCAATGAAGTCGATGCTGATGGCAATGGAACGATTTA 881  | •  |
| Qy                                   | 66                                    | roGluPheArgAsnTrpAlaL   |    |
| DЬ                                   | 882 (                                 | CTTTCCTGAATTTCTTACTATGATGGCTAGAAAAATGAAGGA 923  | _  |
| . Qy                                 | 86                                    | LeuAspSerAspSerIleGlyTrpTyrPheLysTyrLeuAspProAlaGly 10  |    |
| 망                                    | 924 (                                 | CACAGACAGCGAAGAGGAAATCCGAGAAGCATTCCGTGTTTTTGACAAGGATGGGAACGG 983  |    |

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                                                                                            1728 GGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCG 1777
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                                                                                                                         389 roAlaGlyGlySerAlaProThrPheThrValArgValProProSer 405
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                                                                                                                                                                                          ----ThrPheArgGlnValAlaVal-----AspGluValValValThrAsnAsnP
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-677-653A-50 (1-647) x US-09-554-000-7 (1-1971)
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APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/09/554,000
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 08/818,252
PRIOR FILING DATE: 1997-03-14
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                                                                                           GAAAAACTTCATTGCC-
                                                                                                                                                                                                                                   rAsnGluGluCysProValValThrAspValSerValProLeuAspGlyArgGlnTrpSe 154
                                                                                                                                                                                                                                                                                                                              sPheSerValAspAlaGluIleArgGluIle-----Ty 134
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APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT TILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,080
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-11
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               APPLICATION NUMBER: US 60/290,645 FILING DATE: 2001-05-15
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: US-09-917-800A-1543
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PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 11740
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 3112
TYPE: DNA
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                                     APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED:
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 640
LENGTH: 5072
                                                                                                                                                                                                           Sequence 640, Application US/10044090 Patent No. US20020137081A1 GENERAL INFORMATION:
              ORGANISM: Homo
                                   TYPE: DNA
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Applicati
publication No. US2003
GENERAL INFORMATION:
                                                  INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1391
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                                                                                                                                                                                              APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Perfect 8.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                   PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. US20030023075A1el Sequences NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <Unknown>
R APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch. COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
STRANDEDNESS:
                 TYPE:
                                                                                       TELEFAX: (608) 251-9166
                                                                                                                                                               NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Madison
                                LENGTH: 25165
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Plunkett, ou,
Th. Rod
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Best Local Similarity:
Query Match:
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                                                     11953 AGCTCCGGTCTGGCG---GCGGGCAGCAACGTCACGCTGACC-----ATTAACGGG 12000
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251 GluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGlyGlnTyrAlaLeu 270 ::: | | | | | | | | |
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                                                                                    ThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAlaIleThrCys
                                                                                                                          CACGGGCAGGCGCTGGTG-----
                                                                                                                                                         AspThrThrTyrTyrValArgIleArgValLeuArgProThrTyrAspValProAspPro
                                                                                                                                                                                            AATCTCCCCGGTCTGCGGGTCGACACCGTGGCGGCGATGATGTGGTTAATATTATCGAG 11922
                                                                                                                                                                                                                             AsnLeuAlaAspTrpArgTyr---ValValAspSerGluGlnTrpIleAsnPheThrAsn
                                                                                                                                                                                                                                                                   GGTAACGGCACGCGCGAAATCACCATAGACGCG-----
                                                                                                                                                                                                                                                                                                  GluAsn-----LysGluMetSerLeuAspValValAsnAspLeuIleGluTrpLeuAsn 191
                                                                                                                                                                                                                                                                                                                                                                                                         GGCAACGGCGAACTGACCATTTCGGCTTCGGTGACG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrAsnGluGluCysProValValThrAspValSerValProLeuAspGlyArgGlnTrp 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGCCGAAGCGGGCGTGGAACAGACCATCAGCGGGCAGGTGACGGGT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCGCGCTGCCGGGCGTCACCATT----AACGTGGTGGCAACGGACGATATTATTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGGTGCAGGCGAATTTAAGCTGGAGCGTCGATGTTCCGGCCTCCGCGAATTTAAGCTGGAGCGTCGATGTTCCGGCCTCCGCCTACAGGAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleProAspGlyLeuValLysPheSerValAsp-----AlaGluIleArgGluIle 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrLeuAspProAlaGlyAlaThrGluSerAlaArgAlaValGly---GluTyrSerLys 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thr------ValThrPheProAlaAsnIleSerSerMetProGluPheArgAsn
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Matches:
Conservative:
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| 2 -   | 0 ACGGTGACTATCGGCACAAATACCTTTACCACGGTGC   |       | Db X |
|-------|---|-------|------|
| 7     | 4 ThrArgienThrGlvValTvrDroAlaThrAspAspDheAl   | ر.    | 0    |
| 12879 | ** FIRALARISALGOLY WELLEULY SASSICLUCLULLULEUCY SLEUKLAS PASPLEULIS 20 CACGCCCAGGCGCAGATCATCAGCGGCTCCGCCACTGGAGCGGCAACCGGTAGCACCGTG | 1282  | B 3  |
| N     | 6CCGGTCGTCACCATCAACACGGTGGCAGGCGATGATGTGATCAACGCGACGGA  |       | D D  |
| 543   | 1 TrpGluGlyValThrAsnValAsnThrProPheGlyGl  |       | Qγ   |
| 12765 | 15 GCCGGAAACCCGGCCTCGGTTAATCACAACCTGACGGTGGATACGTCCGTT  | 1271  | Db   |
| 530   | 'll ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyrGlnGly  | 51    | Qy   |
| 12714 |   | 1265  | Db   |
| 510   | 1 ArgAspLeuProAspTyrThrGlyIleArgAspSerPheAspGlnAsnMet   | 49    | Qy   |
| 12654 | 5 GGCACAAACTACACCGGCACCGTACAGACGGACGGCAGCTGGAGCGTCAGCGTACCGTCA  | 1259  | рь   |
| 490   | 4 AsnProGlyTyrGluArgThr   | 48    | Qy   |
| 12594 | 0   | 1258  | Db   |
| 483   | 4 MetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaValSerPheAsn  | 46    | Qy   |
| 12579 | 99  | 1257  | ДЬ   |
| 463   | 44 ProLysIleGluGlnSerLeuLeuLysGluThrLeuGlyCysTyrLeuValHisSerLys   | 44    | Qy   |
| 12579 | P GCGCCTCTGACCATCACCGGCAGCACGCGCGAGACGGGGCAGACGGTG  | 1252  | Db   |
| 443   | 5 ArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrValAlaAsnAsn   | 42    | Qy   |
| 12528 | 4AATACCATTGCGGGCGATGATATTCTTAACGCCGG  | 1248  | 뭕    |
| 424   | 5 SerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuGluThrArgProSerSer  | 40    | Qy   |
| 12483 |   | 1243  | В    |
| 404   | 5 ValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrValArgValProPro  | 38    | Qy   |
| 12435 |   | 1237  | Db   |
| 384   | 6 ArgGinValAlaValAspGluVal  | 37    | Qy   |
| 12375 | 6 ACGGTGGCTGCGAATGGTTCCTGGAGCACCTCGGTTCCGGCGGCAGATATGGCGGCTCTG  | 1231  | DЬ   |
| 375   | 6 TyrAs   | 35    | Qy   |
| 12315 | FILE TOTGGCGTTGAAGCCGACAAACGGTTACCGTCACCTTTGGCGGCAAAACTTACAGCGCC  | 1225  | Db   |
| 355   | 6 ThrThrPheProAlaGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArg  | 33    | Qy   |
| 12255 | 6 GCCGATGATGTGATCAACGCTGCCGAAAAAAGGCGCGGCGTTAACGCTCTCCGGCAGCACC   | 1219  | 망    |
| 335   | 6 GlyThrProAlaTrpGluGlnAlaSerSerGlyGlyTyrLeuThrTrpArgHisAsnGly  | 31    | Qy   |
| 12195 | 6 GTTACGCATCCGGTGACGGTCGATCTCTCGGCGGTGGCGGTGAGCATCAACGCCATTACC  | 1213  | рь   |
| 315   | GlyThrAlaProAla   | 311   | Qy   |
| 12135 | 4 ATTGCGGCGAGCGGTAGCACCTCT  | 1209  | р    |
| 310   | 1 PheAlaArgProSerSerAlaAlaAlaLeuAlaPheValTrpAlaGlyLeuProGlnGly  | 29    | Qy   |
| 12093 | 9GTTCCGGCGGTGGATGTCAGCGCCTGCCGGGATCGGTGACG  | ₽-    | ф    |
| 290   | 1 ThrProThrSerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHisThrLeuThr  | 27    | Qy   |
| 12048 | CAAACCTATGTTGCGGCGGTGCTGGCGGATGGCACCTGGAGCGTCGGC  | 12001 | рь   |

| Qy<br>VQ  | Оу  | Оу  | Qу  | Qy<br>Db  |
|---|---|---|---|---|
| 632<br>13147  | 629<br>13087  | 616<br>13028                              | 598<br>12991  | 578<br>12940  |
| 632 aArgvalArgAlaArgArgAlaArgArgAlaAlaAlaArgAla 646<br> | 629LysIleAlaAl 632 13087 ATCAGCGGCGATAACATCCTGAACGCCGATGAAAAAGGCCAGCCGTTGACCATCAGCGGC 13146 | 616 uAlaLysLeuProGlyLeuLeuMetSerValProGly | 598SerSerIleIleLysSerValGly-GluThrAlaValGlyAlaAlaGlnSerGlyLe 6 :::::: | Qy 578 AlahlavalSerAlapheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThr 597 |
|   | 3146  | 628<br>13086                              | 616<br>13027  | 597<br>12990  |

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